

Figure 1

1 * 10 * 20 * 30 *
 G AATTCCGCTA CTACTCAACA ATG AAG ATG CTT TAC GCT ATC GCT
 Met Lys Met Leu Tyr Ala Ile Ala

 40 * 50 * 60 * 70 *
 ATA ATG TTT CTC CTG GTA TCA TTA TGC AGC GCA AGA ACA GTG
 Ile Met Phe Leu Leu Val Ser Leu Cys Ser Ala Arg Thr Val

 80 * 90 * 100 * 110 * 120 *
 AGG AAG GCA TAC CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC
 Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp

 130 * 140 * 150 * 160 *
 GAC TGT GGA ACT CAG AAG CCA TGC GAG GCC AAG TGC AAT GAG
 Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu

 170 * 180 * 190 * 200 *
 GAA CCC CCT GAG GAG GAA GAT CCG ATA TGC CGC TCA CGT GGT
 Glu Pro Pro Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly

 210 * 220 * 230 * 240 *
 TGT TTA TTA CCT CCT GCT TGC GTA TGC AAA GAC GGA TTC TAC
 Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr

 250 * 260 * 270 * 280 *
 AGA GAC ACG GTG ATC GGC GAC TGT GTT AGG GAA GAA GAA TGC
 Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Cys

 290 * 300 * 310 * 320 * 330 *
 GAC CAA CAT GAG ATT ATA CAT GTC TGA ACGAGAAAGC AACAAATAACC
 Asp Gln His Glu Ile Ile His Val

 340 * 350 * 360 * 370 * 380 *
 AAAGGTTCCA ACTCTCGCTC TGCAAAATCG CTAGTTGGAT GTCTCTTTG

 390 * 400 * 410 * 420 * 430 *
 CGTCCGAATA GTTTAGTTG ATGTTAAGTA AGAACTCCTG CTGGAGAGAA

 440 * 450 *
 TAAAGCTTTC CAACTCC poly(A)

Figure 2

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp
1 5 10

Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu Glu
15 20 25

Pro Pro Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly Cys
30 35 40

Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg
45 50 55

Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Cys Asp
60 65 70

Gln His Glu Ile Ile His Val
75

Figure 3

1 * 10 * 20 * 30 *
 G AATTCCGCTA CTACTCAACA ATG AAG ATG CTT TAC GCT ATC GCT
 Met Lys Met Leu Tyr Ala Ile Ala
 40 * 50 * 60 * 70 *
 ATA ATG TTT CTC CTG GTG TCA TTA TGC AGC ACA AGA ACA GTG
 Ile Met Phe Leu Leu Val Ser Leu Cys Ser Thr Arg Thr Val
 80 * 90 * 100 * 110 * 120 *
 AGG AAG GCA TAC CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC
 Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp
 130 * 140 * 150 * 160 *
 GTC TGT GGA ACT AAG AAG CCA TGC GAG GCC AAG TGC AGT GAG
 Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu
 170 * 180 * 190 * 200 *
 GAA GAG GAG GAA GAT CCG ATA TGC CGA TCA TTT TCT TGT CCG
 Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro
 210 * 220 * 230 * 240 *
 GGT CCC GCT GCT TGC GTA TGC GAA GAC GGA TTC TAC AGA GAC
 Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp
 250 * 260 * 270 * 280 *
 ACG GTG ATC GGC GAC TGT GTT AAG GAA GAA GAA TGC GAC CAA
 Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys Asp Gln
 290 * 300 * 310 * 320 * 330 *
 CAT GAG ATT ATT CAT GTC TGA ACGAGAGAGC AGTAATAACC
 His Glu Ile Ile His Val
 340 * 350 * 360 * 370 * 380 *
 AAAGGTTCCA ACTTTCGCTC TACAAAATCG CTAGTTGGAT TTCTCCTTG
 390 * 400 * 410 * 420 * 430 *
 CGTGCGAATA GTTTAGTTG ATATTAAGTA AAACCTCCTG TTGAAGAGAA
 440 *
 TAAAGCTTTC CAACTTC poly(A)

Figure 4

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Val
1 5 10

Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu
15 20 25

Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly
30 35 40

Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr
45 50 55

Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys Asp Gln His
60 65 70

Glu Ile Ile His Val
75

Figure 5

Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu
1 5 10

Trp Leu Asp Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys
15 20

Cys Asn Glu Glu Pro Pro Glu Glu Asp Pro Ile Cys Arg
25 30 35

Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp
40 45 50

Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu
55 60 65

Glu Glu Cys Asp Gln His Glu Ile Ile His Val
70 75

Figure 6

Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu
1 5 10

Trp Leu Asp Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys
15 20

Cys Ser Glu Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe
25 30 35

Ser Cys Pro Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe
40 45 50

Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu
55 60 65

Cys Asp Gln His Glu Ile Ile His Val
70 75

Figure 7A-1

1	10	20	30	40
*	*	*	*	*
<u>GAATTCACTA</u>	TTATCCAACA	ATG GCG GTG CTT TAT TCA GTA GCA		
ECORI		Met Ala Val Leu Tyr Ser Val Ala		
50	60	70	80	
*	*	*	*	
ATA GCG TTA CTA CTG GTA TCA CAA TGC AGT GGG AAA CCG AAC				
Ile Ala Leu Leu Val Ser Gln Cys Ser Gly Lys Pro Asn				
90	100	110	120	
*	*	*	*	
AAT GTG ATG ACT AAC GCT TGT GGT CTT AAT GAA TAT TTC GCT				
Asn Val Met Thr Asn Ala Cys Gly Leu Asn Glu Tyr Phe Ala				
130	140	150	160	170
*	*	*	*	*
GAG TGT GGC AAT ATG AAG GAA TGC GAG CAC AGA TGC AAT GAG				
Glu Cys Gly Asn Met Lys Glu Cys Glu His Arg Cys Asn Glu				
180	190	200	210	
*	*	*	*	
GAG GAA AAT GAG GAA AGG GAC GAG GAA AGA ATA ACG GCA TGC				
Glu Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile Thr Ala Cys				
220	230	240	250	
*	*	*	*	
CTC ATC CGT GTG TGT TTC CGT CCT GGT GCT TGC GTA TGC AAA				
Leu Ile Arg Val Cys Phe Arg Pro Gly Ala Cys Val Cys Lys				
260	270	280	290	
*	*	*	*	
GAC GGA TTC TAT AGA AAC AGA ACA GGC AGC TGT GTG GAA GAA				
Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser Cys Val Glu Glu				
300	310	320	330	
*	*	*	*	
GAT GAC TGC GAG TAC GAG AAT ATG GAG TTC ATT ACT TTT GCA				
Asp Asp Cys Glu Tyr Glu Asn Met Glu Phe Ile Thr Phe Ala				
340	350	360	370	380
*	*	*	*	*
CCA GAA GTA CCG ATA TGT GGT TCC AAC GAA AGG TAC TCC GAC				
Pro Glu Val Pro Ile Cys Gly Ser Asn Glu Arg Tyr Ser Asp				
390	400	410	420	
*	*	*	*	
TGC GGC AAT GAC AAA CAA TGC GAG CGC AAA TGC AAC GAG GAC				
Cys Gly Asn Asp Lys Gln Cys Glu Arg Lys Cys Asn Glu Asp				
430	440	450	460	
*	*	*	*	
GAT TAT GAG AAG GGA GAT GAG GCA TGC CGC TCA CAT GTT TGT				
Asp Tyr Glu Lys Gly Asp Glu Ala Cys Arg Ser His Val Cys				

Figure 7A-2

470	480	490	500	
*	*	*	*	
GAA CGT CCT GGT GCC TGT GTA TGC GAA GAC GGG TTC TAC AGA				
Glu Arg Pro Gly Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg				
510	520	530	540	
*	*	*	*	
AAC AAA AAA GGT AGC TGT GTG GAA AGC GAT GAC TGC GAA TAC				
Asn Lys Lys Gly Ser Cys Val Glu Ser Asp Asp Cys Glu Tyr				
550	560	570	580	590
*	*	*	*	*
GAT AAT ATG GAT TTC ATC ACT TTT GCA CCA GAA ACC TCA CGA				
Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu Thr Ser Arg				
600	610	620	630	640
*	*	*	*	*
TAA CCAAAGATGC TACCTCTCGT ACGCAACTCC GCTGATTGAGGTTGATTG				
650	660	670	680	690
*	*	*	*	*
ACTCCCTTGCATCTAACATTTTTTGATGCTGTCATCTGAGCTAACCTG				
700	710			
*	*			
ATAAAGCCTATGGTG poly(A)				

Figure 7B

1 10 20 30 40
 * * * * *
GAATTCCGC ATG CGG ACG CTC TAC CTC ATT TCT ATC TGG TTG
 EcoRI Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu

 50 60 70 80
 * * * *
 TTC CTC ATC TCG CAA TGT AAT GGA AAA GCA TTC CCG AAA TGT
 Phe Leu Ile Ser Gln Cys Asn Gly Lys Ala Phe Pro Lys Cys

 90 100 110 120
 * * * *
 GAC GTC AAT GAA AGA TTC GAG GTG TGT GGC AAT CTG AAG GAG
 Asp Val Asn Glu Arg Phe Glu Val Cys Gly Asn Leu Lys Glu

 130 140 150 160
 * * * *
 TGC GAG CTC AAG TGC GAT GAG GAC CCT AAG ATA TGC TCT CGT
 Cys Glu Leu Lys Cys Asp Glu Asp Pro Lys Ile Cys Ser Arg

 170 180 190 200 210
 * * * * *
 GCA TGT ATT CGT CCC CCT GCT TGC GTA TGC GAT GAC GGA TTC
 Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp Asp Gly Phe

 220 230 240 250
 * * * *
 TAC AGA GAC AAA TAT GGC TTC TGT GTT GAA GAA GAC GAA TGT
 Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu Asp Glu Cys

 260 270 280 290
 * * * *
 AAC GAT ATG GAG ATT ATT ACT TTT CCA CCA GAA ACC AAA TGA
 Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys

 300 310 320 330 340
 * * * * *
 TGACCGAACGC TTCCACCTTT CTATACATAT CTTCACTGCTTGACAGGGCTCT

 350 360 370 380 390 400
 * * * * * *
 CGACAATTTAGAAGTTCTGCTTGACTTTGCTATTGAAATTGTTCACACTAATG

 410 420
 * *
 GGGGAAGTAAAGCATTTCACGAC poly(A)

Figure 7C

1	10	20	30	40
*	*	*	*	*
<u>GAATTCCGCT</u>	ACATTTCAA	CA ATG TCG ACG CTT TAT GTT ATC		
EcoRI		Met Ser Thr Leu Tyr Val Ile		
50	60	70	80	
*	*	*	*	
GCA ATA TGT TTG CTG CTT GTT TCG CAA TGC AAT GGA AGA ACG				
Ala Ile Cys Leu Leu Val Ser Gln Cys Asn Gly Arg Thr				
90	100	110	120	
*	*	*	*	
GTG AAG AAG TGT GGC AAG AAT GAA AGA TAC GAC GAC TGT GGC				
Val Lys Lys Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly				
130	140	150	160	
*	*	*	*	
AAT GCA AAG GAC TGC GAG ACC AAG TGC GGT GAA GAG GAA AAG				
Asn Ala Lys Asp Cys Glu Thr Lys Cys Gly Glu Glu Glu Lys				
170	180	190	200	210
*	*	*	*	*
GTG TGC CGT TCG CGT GAG TGT ACT AGT CCT GGT GCC TGC GTA				
Val Cys Arg Ser Arg Glu Cys Thr Ser Pro Gly Ala Cys Val				
220	230	240	250	
*	*	*	*	
TGC GAA CAA GGA TTC TAC AGA GAT CCG GCT GGC GAC TGT GTC				
Cys Glu Gln Gly Phe Tyr Arg Asp Pro Ala Gly Asp Cys Val				
260	270	280	290	
*	*	*	*	
ACT GAT GAA GAA TGT GAT GAA TGG AAC AAT ATG GAG ATC ATT				
Thr Asp Glu Glu Cys Asp Glu Trp Asn Asn Met Glu Ile Ile				
300	310	320	330	340
*	*	*	*	*
ACT ATG CCA AAA CAG TAG TGCGAAGTTC CCTTCTTTCT CCAAATCTG				
Thr Met Pro Lys Gln				
350	360	370	380	390
*	*	*	*	*
C TCCGTGCTCAATTATCACACACCTCCACTAGTTAAGATTGACTGACTCTCTTG				
400	410	420	430	440
*	*	*	*	*
CATTGTAGTATTTCGCTGACTCTGTGCATTTAAGCATGAGATACTACTAGGGA				
450				
460	470			
*	*			
GAATAAAAATTACTAACTAC	poly(A)			

Figure 7D

1 10 20 30 40
 * * * * *
GAATTCCGG AAA TGT CCT ACC GAT GAA TGG TTC GAT TGG TGT
 EcoRI Lys Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys
 50 60 70 80
 * * * *
 GGA ACT TAC AAG CAT TGC GAA CTC AAG TGC GAT AGG GAG CTA
 Gly Thr Tyr Lys His Cys Glu Leu Lys Cys Asp Arg Glu Leu
 90 100 110 120
 * * * *
 ACT GAG AAA GAA GAG CAG GCA TGT CTC TCA CGT GTT TGT GAG
 Thr Glu Lys Glu Glu Gln Ala Cys Leu Ser Arg Val Cys Glu
 130 140 150 160
 * * * *
 AAG TCC GCT TGC GTA TGC AAT GAC GGA TTA TAC AGA GAC AAG
 Lys Ser Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Lys
 170 180 190 200 210
 * * * * *
 TTT GGC AAC TGT GTT GAA AAA GAC GAA TGC AAC GAT ATG GAG
 Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu
 220 230 240 250
 * * * *
 ATT ATT ACT TTT GCA CCA GAA ACC AAA TAA TGGCCTAAGG TTCC
 Ile Ile Thr Phe Ala Pro Glu Thr Lys
 260 270 280 290 300
 * * * * *
 AAACCT TGCTACACAC CGTCAGTGCTTACTGTTCTCTACGTGTTAGTAGT
 310 320 330 340 350 360
 * * * * * *
 TTTGCTTGACTCTGTGTATTAAGCATTGTCTACTAATGGGCAAAGTAAAGCATT
 370 380 390
 * * *
 GTAAGGACATAATAATGAGTAAACCTCTGATTT poly(A)

Figure 7E-1

1	10	20	30	40
*	*	*	*	*
<u>GAATTCCGGG</u>	CGGCAGAAAG	ATG CGA ATG CTC TAC CTT GTT CCT		
EcoRI		Met Arg Met Leu Tyr Leu Val Pro		
50	60	70	80	
*	*	*	*	
ATC	TGG TTG CTG CTC ATT TCG CTA TGC AGT GGA AAA GCT GCG			
Ile	Trp Leu Leu Ile Ser Leu Cys Ser Gly Lys Ala Ala			
90	100	110	120	
*	*	*	*	
AAG AAA TGT GGT CTC AAT GAA AGG CTG GAC TGT GGC AAT CTG				
Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn Leu				
130	140	150	160	170
*	*	*	*	*
AAG CAA TGC GAG CCC AAG TGC AGC GAC TTG GAA AGT GAG GAG				
Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu				
180	190	200	210	
*	*	*	*	
TAT GAG GAG GAA GAT GAG TCG AAA TGT CGA TCA CGT GAA TGT				
Tyr Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys				
220	230	240	250	
*	*	*	*	
TCT CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC TAC AGA AAC				
Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn				
260	270	280	290	
*	*	*	*	
AAG AAG GGC AAG TGT GTT GCA AAA GAT GTT TGC GAG GAC GAC				
Lys Lys Gly Lys Cys Val Ala Lys Asp Val Cys Glu Asp Asp				
300	310	320	330	
*	*	*	*	
AAT ATG GAG ATT ATC ACT TTT CCA CCA GAA GAC GAA TGT GGT				
Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Glu Cys Gly				
340	350	360	370	380
*	*	*	*	*
CCC GAT GAA TGG TTC GAC TAC TGT GGA AAT TAT AAG AAG TGC				
Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys Lys Cys				
390	400	410	420	
*	*	*	*	
GAA CGC AAG TGC AGT GAG GAG ACA AGT GAG AAA AAT GAG GAG				
Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Glu				
430	440	450	460	
*	*	*	*	
GCA TGC CTC TCT CGT GCT TGT ACT GGT CGT GCT TGC GTA TGC				
Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys				

Figure 7E-2

470 480 490 500
* * * *
AAA GAC GGA TTG TAC AGA GAC GAC TTT GGC AAC TGT GTT CCA
Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro

510 520 530 540
* * * *
CAT GAC GAA TGC AAC GAT ATG GAG ATC ATC ACT TTT CCA CCG
His Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro

550 560 570 580 590
* * * * *
GAA ACC AAA CAT TGA CCAGAGGCTC CAACTCTCGC TACACAAACGT CA
Glu Thr Lys His

600 610 620 630 640 650
* * * * * *
GGGCTAGAATGGCCCTCTGCGAGTTAGTAGTTTGCTTGACTCTGCTTATTTGA

660 670 680
* * *

GCACTTCTATTGATGGCGAAAATAAAGCATTAAAAC poly(A)

Figure 7F

1 10 20 30 40
 * * * * *
GAATTCCGCG CACCTGAGAG GTGAGCTACG CAAGTCTTCG CTGGTACA
 EcoRI

50 60 70 80 90
 * * * * *
 ATG ATC CGA AAG CTC GTT CTG CTG ACT GCT ATC GTC ACG GTG
 Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Thr Val

100 110 120 130
 * * * *
 GTG CTA AGT GCG AAG ACC TGT GGA CCA AAC GAG GAG TAC ACT
 Val Leu Ser Ala Lys Thr Cys Gly Pro Asn Glu Glu Tyr Thr

140 150 160 170
 * * * *
 GAA TGC GGG ACG CCA TGC GAG CCG AAG TGC AAT GAA CCG ATG
 Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Glu Pro Met

180 190 200 210
 * * * *
 CCA GAC ATC TGT ACT CTG AAC TGC ATC GTG AAC GTG TGT CAG
 Pro Asp Ile Cys Thr Leu Asn Cys Ile Val Asn Val Cys Gln

220 230 240 250
 * * * *
 TGC AAA CCC GGC TTC AAG CGC GGA CCG AAA GGA TGC GTC GCC
 Cys Lys Pro Gly Phe Lys Arg Gly Pro Lys Gly Cys Val Ala

260 270 280 290 300
 * * * * *
 CCC GGA CCA GGC TGT AAA TAG TTCTCCACCT GCCCTTCGT TGGAA
 Pro Gly Pro Gly Cys Lys

310 320 330 340
 * * * *
 CAAAT GGCTGTCTTTACATTCTGAATCAATAAGCCGAACGGT poly(A)

Figure 8A

1	10	20	30	40
*	*	*	*	*
<u>AAGCTTTGCT</u> AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT				
HindIII Met Pro Val				
50	60	70	80	90
*	*	*	*	*
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT				
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu				
100	110	120	130	
*	*	*	*	*
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG				
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys				
140	150	160	170	
*	*	*	*	*
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT				
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala				
180	190	200	210	
*	*	*	*	*
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT				
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser				
220	230	240	250	
*	*	*	*	*
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT				
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val				
260	270	280	290	300
*	*	*	*	*
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT				
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val				
310	320	330	340	
*	*	*	*	*
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA				
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys				
350	360	370	380	
*	*	*	*	*
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC				
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly				
390	400	410	420	430
*	*	*	*	*
TCA GGC GGA <u>GGCCAAGTCGGCC</u> ATCCCATATCAC <u>GCGGCCGC</u> <u>GGATCC</u>				
Ser Gly Gly SfI NotI BamHI				

Figure 8B

1	10	20	30	40
*	*	*	*	*
<u>AAGCTTGCT</u> AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT				
HindIII Met Pro Val				
50	60	70	80	90
*	*	*	*	*
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT				
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu				
100	110	120	130	
*	*	*	*	*
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG				
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys				
140	150	160	170	
*	*	*	*	*
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT				
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala				
180	190	200	210	
*	*	*	*	*
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT				
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser				
220	230	240	250	
*	*	*	*	*
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT				
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val				
260	270	280	290	300
*	*	*	*	*
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT				
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val				
310	320	330	340	
*	*	*	*	*
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA				
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys				
350	360	370	380	
*	*	*	*	*
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC				
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly				
390	400	410	420	430
*	*	*	*	*
TCA GGC GGA G <u>GGCCAAGTCGGCC</u> ATCCCATATCAC <u>GCGGCCGC</u> GGATCC				
Ser Gly Gly SfiI NotI BamHI				

Figure 8c

1	10	20	30	40
*	*	*	*	*
<u>AAGCTTTGCT</u> AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT				
HindIII Met Pro Val				
50	60	70	80	90
*	*	*	*	*
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT				
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu				
100	110	120	130	
*	*	*	*	*
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG				
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys				
140	150	160	170	
*	*	*	*	*
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT				
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala				
180	190	200	210	
*	*	*	*	*
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT				
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser				
220	230	240	250	
*	*	*	*	*
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT				
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val				
260	270	280	290	300
*	*	*	*	*
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT				
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val				
310	320	330	340	
*	*	*	*	*
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA				
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys				
350	360	370	380	
*	*	*	*	*
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC				
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly				
390	400	410	420	430
*	*	*	*	*
TCA GGC GGA TC <u>GGCCAAGTCGGCC</u> ATCCCATATCAC <u>GCGGCCGC</u> <u>GGATCC</u>				
Ser Gly Gly SfiI NotI BamHI				

Figure 9

1 10 20 30 40
 * * * * *
GAATTCCGG CTG GTW TCC TAC TGC AGT GGA AAA GCA ACG ATG
 EcoRI Leu Val Ser Tyr Cys Ser Gly Lys Ala Thr Met

 50 60 70 80
 * * * *
 CAG TGT GGT GAG AAT GAA AAG TAC GAT TCG TGC GGT AGC AAG
 Gln Cys Gly Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys

 90 100 110 120
 * * * *
 GAG TGC GAT AAG AAG TGC AAA TAT GAC GGA GTT GAG GAG GAA
 Glu Cys Asp Lys Lys Cys Lys Tyr Asp Gly Val Glu Glu Glu

 130 140 150 160
 * * * *
 GAC GAC GAG GAA CCT AAT GTG CCA TGC CTA GTA CGT GTG TGT
 Asp Asp Glu Glu Pro Asn Val Pro Cys Leu Val Arg Val Cys

 170 180 190 200 210
 * * * * *
 CAT CAA GAT TGC GTA TGC GAA GAA GGA TTC TAT AGA AAC AAA
 His Gln Asp Cys Val Cys Glu Gly Phe Tyr Arg Asn Lys

 220 230 240 250
 * * * *
 GAT GAC AAA TGT GTA TCA GCA GAA GAC TGC GAA CTT GAC AAT
 Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu Leu Asp Asn

 260 270 280 290
 * * * *
 ATG GAC TTT ATA TAT CCC GGA ACT CGA AAC TGA ACGAAGGCTC
 Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn

 300 310 320 330 340
 * * * * *
 CATTCTTGCT GCACAAGATC GATTGTCTCTCCCTGCATCTCAGTAGTTTGC

 350 360 370 380 390 400
 * * * * * *
 TACATTGTATATGGTAGCAAAAAATTAGCTTAGGGAGAATAAAATCTTACCTAT

 410 420 430
 * * *
 ATTTAATCAATGAAGTATTCTCTTCT poly(A)

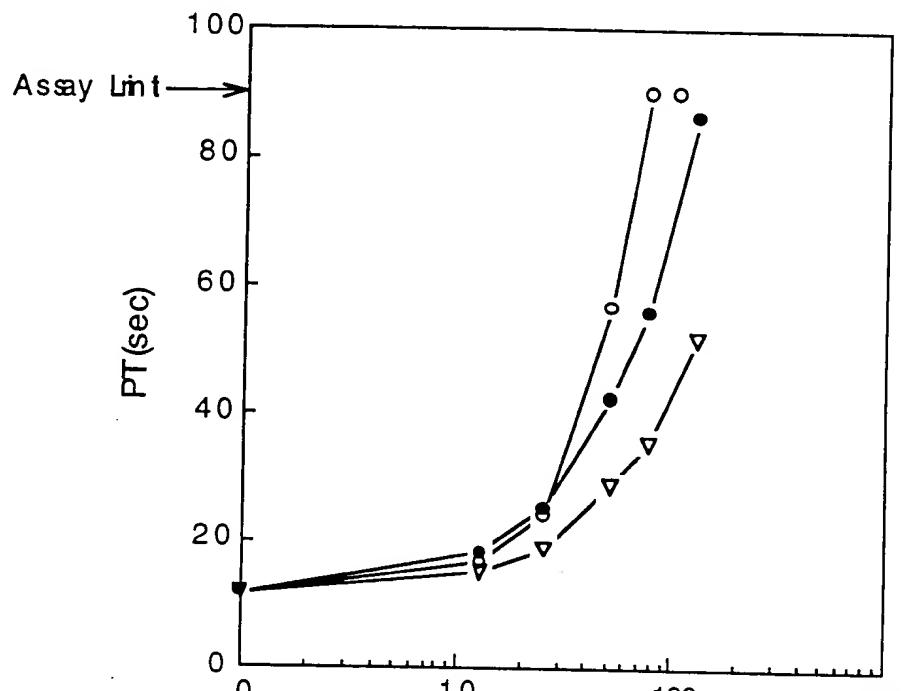
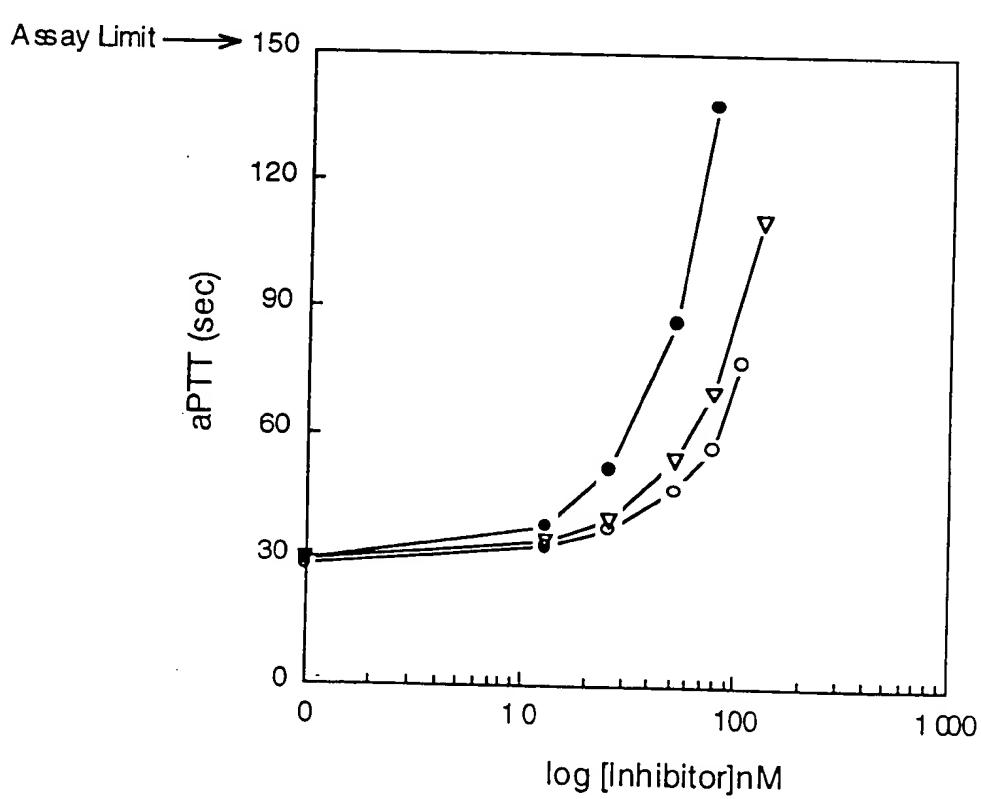
Figure 10**A.****B.**

Figure 11-1

NAP5	Met Lys Met Leu Tyr Ala Ile Ala Ile Met Phe Leu Leu Val
NAP6	Met Lys Met Leu Tyr Ala Ile Ala Ile Met Phe Leu Leu Val
NAPc2	
AcenAP5	Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu Phe Leu Ile
AcenAP7	Met Ser Thr Leu Tyr Val Ile Ala Ile Cys Leu Leu Leu Val
AcenAP4d1	Met Ala Val Leu Tyr Ser Val Ala Ile Ala Leu Leu Leu Val
AcenAP4d2	
AduNAP4	
AduNAP7d1	Met Arg Met Leu Tyr Leu Val Pro Ile Trp Leu Leu Leu Ile
AduNAP7d2	
HponAP5	Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Thr

Figure 11-2

Figure 11-3

		¹	²
NAP5		CYS GLY Glu Asn Glu Trp Leu Asp Asp CYS Gly Thr Gln	
NAP6		CYS GLY Glu Asn Glu Trp Leu Asp Val CYS Gly Thr Lys	
NAPc2		CYS GLY Glu Asn Glu Lys Tyr Asp Ser CYS Gly Ser Lys	
AcenNAP5		CYS Asp Val Asn Glu Arg Phe Glu Val CYS Gly Asn Leu	
AcenNAP7		CYS Gly Lys Asn Glu Arg Tyr Asp Asp CYS Gly Asn Ala	
AcenNAP4d1		CYS Gly Leu Asn Glu Tyr Phe Ala Glu CYS Gly Asn Met	
AcenNAP4d2		CYS Gly Ser Asn Glu Arg Tyr Ser Asp CYS Gly Asn Asp	
AduNAP4		CYS Pro Thr Asp Glu Trp Phe Asp Trp CYS Gly Thr Tyr	
AduNAP7d1		CYS Gly Leu Asn Glu Arg Leu Asp --- CYS Gly Asn Leu	
AduNAP7d2		CYS Gly Pro Asp Glu Trp Phe Asp Tyr CYS Gly Asn Tyr	
HpoNAP5		CYS Gly Pro Asn Glu Glu Tyr Thr Glu CYS Gly Thr ---	

Figure 11-4

NAP5		Lys	Pro	Cys	3	Glu	Ala	Lys	Cys	4														
NAP6		LYS	Pro	CYS		GLU	ALA	LYS	CYS		---	---	---	---	---	---	---	---	---	---	---	Asn	Glu	Glu
NAPc2		Glu	---	Cys		Asp	Lys	Lys	Cys		---	---	---	---	---	---	---	---	---	---	---	Ser	Glu	Glu
AcenAP5		LYS	Glu	CYS		GLU	LEU	LYS	CYS		---	---	---	---	---	---	---	---	---	---	---			
AcenAP7		LYS	ASP	CYS		GLU	THR	LYS	CYS		---	---	---	---	---	---	---	---	---	---	---	Gly	---	---
AcenAP4d1		LYS	Glu	CYS		GLU	HIS	Arg	CYS	Asn	GLU	GLU	GLU	Asn	GLU									
AcenAP4d2		LYS	Gln	CYS		GLU	Arg	Lys	CYS	Asn	GLU	ASP	ASP	Tyr	Glu	Lys								
AdunAP4		LYS	His	CYS		GLU	Leu	LYS	CYS	ASP	Arg	GLU	Leu	Thr	Glu	Lys								
AdunAP7d1		LYS	Gln	CYS		GLU	Pro	LYS	CYS	Ser	Asp	Leu	Glu	Ser	Glu	Glu								
AdunAP7d2		LYS	LYS	CYS		GLU	Arg	Lys	CYS	Ser	GLU	GLU	THR	Ser	Glu	Glu	LYS							
HpoNAP5		---	Pro	CYS		GLU	Pro	LYS	CYS	---	---	---	---	---	---	---	---	---	---	---	---			

Figure 11-5

NAP5	Pro	Pro	Glu	Glu	Glu	Asp	Pro	Ile	---	---	5	Cys	Arg	Ser	Arg		
NAP6	-	-	-	Glu	Glu	Glu	Asp	Pro	Ile	---	---	Cys	Arg	Ser	Phe		
NAPc2	-	-	Glu	Asp	Asp	Glu	Glu	Pro	Asn	Val	Pro	Cys	Leu	Val	Arg		
AcenNAP5	-	-	-	Asp	Glu	Asp	Pro	Lys	Ile	---	---	Cys	---	Ser	Arg		
AcenNAP7	-	-	-	Glu	Glu	Glu	-	---	LYS	-	-	Val	-	-	Cys		
AcenNAP4d1	Arg	-	-	Asp	Glu	Glu	-	-	Arg	Ile	Thr	Ala	Cys	Leu	Ile	Arg	
AcenNAP4d2	Gly	-	-	Asp	Glu	-	-	-	-	-	-	-	Ala	Cys	Arg	Ser	His
AduNAP4	-	-	-	Glu	Glu	-	-	-	Gln	-	-	-	Ala	Cys	Leu	Ser	Arg
AduNAP7d1	Tyr	-	-	Glu	Glu	Glu	Asp	Glu	Ser	Lys	-	-	Cys	Arg	Ser	Arg	
AduNAP7d2	Asn	-	-	Glu	Glu	-	-	-	-	-	-	-	Ala	Cys	Leu	Ser	Arg
HpoNAP5	-	-	-	Asn	Glu	Pro	Met	Pro	Asp	Ile	-	-	Cys	-	-	Thr	Leu

Figure 11-6

NAP5	Gly	Cys ⁶	Leu	Leu	Pro	Pro	Ala	Cys ⁷	Val	Cys ⁸	Lys	Asp
NAP6	Ser	Cys	Pro	Gly	Pro	Ala	Ala	Cys	Val	Cys	Glu	Asp
NAPc2	Val	Cys	His	Gln	Asp	---	---	Cys	Val	Cys	Glu	Glu
AcenNAP5	Ala	Cys	Ile	Arg	Pro	Pro	Ala	Cys	Val	Cys	Asp	Asp
AcenNAP7	Glu	Cys	Thr	Ser	Pro	Gly	Ala	Cys	Val	Cys	Glu	Gln
AcenNAP4d1	Val	Cys	Phe	Arg	Pro	Gly	Ala	Cys	Val	Cys	Lys	Asp
AcenNAP4d2	Val	Cys	Glu	Arg	Pro	Gly	Ala	Cys	Val	Cys	Glu	Asp
AduNAP4	Val	Cys	Glu	Lys	---	Ser	Ala	Cys	Val	Cys	Asn	Asp
AduNAP7d1	Glu	Cys	Ser	Arg	Arg	---	Val	Cys	Val	Cys	Asp	Glu
AduNAP7d2	Ala	Cys	Thr	Gly	Arg	---	Ala	Cys	Val	Cys	Lys	Asp
HpoNAP5	Asn	Cys	Ile	Val	Asn	---	Val	Cys	Gln	Cys	Lys	Pro

Figure 11-7

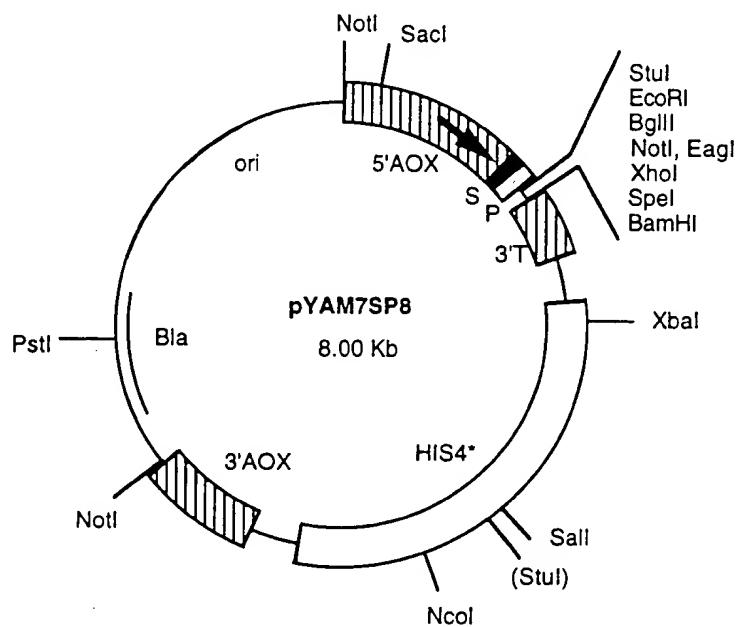
NAP5	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	⁹ C	Y	S	V	A	R	G	l	u
NAP6	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	C	Y	S	V	A	L	Y	S	G
NAPc2	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	C	Y	S	V	A	S	E	A	l
AceNAP5	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	C	Y	S	V	A	G	l	u	G
AceNAP7	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	L	Y	T	R	Y	G	l	u	G
AceNAP4d1	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	Y	R	A	S	P	C	Y	S	V
AceNAP4d2	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	Y	R	A	S	P	C	Y	S	V
AduNAP4	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	Y	R	A	S	P	C	Y	S	V
AduNAP7d1	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	Y	R	A	S	P	C	Y	S	V
AduNAP7d2	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	Y	R	A	S	P	C	Y	S	V
HponAP5	G	L	Y	P	h	E	T	Y	R	A	g	A	S	P	Y	R	A	S	P	C	Y	S	V

Figure 11-8

Figure 11-9

NAP5	Val	end
NAP6	Val	end
NAPc2	Pro	Gly
	Thr	Arg
	Asn	end
AceNAP5	Phe	Pro
	Pro	Glu
	Thr	Lys
		end
AceNAP7	Met	Pro
	Lys	Gln
		end
AceNAP4d1	Phe	Ala
	Pro	Glu
AceNAP4d2	Phe	Ala
	Pro	Glu
	Thr	Ser
	Arg	end
AduNAP4	Phe	Ala
	Pro	Glu
	Thr	Lys
		end
AduNAP7d1	Phe	Pro
	Pro	Glu
AduNAP7d2	Phe	Pro
	Pro	Glu
	Thr	Lys
	His	end
HponNAP5		

Figure 12

A**B**

<----5'AOX1-----><-----PHO1 secretion signal (S)-----
TTATTCGAAACGATGTTCTCTCCAATTTGTCCTGGAAATTATTTA

-----><----Pro Sequence (P)-----
 GCTACTTGCAATCTGTCTCGCCCAGCCAGTTATCTCCACTACCGTTGGTCC

-----><--Multi-Cloning Site (MCS)
 GCTGCCGAGGGTTCTTGGACAAGAGGCCTATCCGCGGAATTCAAGATCTGAAT
 StuI SacII EcoRI BglII

-----><---3' T--->
 GCGGCCGCTCGAGACTAGTGGATCCTTAGACA...
 NotI XhoI SpeI BamHI
 EagI

Figure 13 A-1 (AcaNAP23)

10	20	30	40	
*	*	*	*	
<u>GAATTCCGCG</u> GAATTCCGCT TGCTACTACT CAACG ATG AAG ACG CTC				
EcoRI Met Lys Thr Leu				
50	60	70	80	
*	*	*	*	
TAT ATT GTC GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT				
Tyr Ile Val Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr				
90	100	110	120	130
*	*	*	*	*
GGA AAA CCT TCG GAG AAA GAA TGT GGT CCC CAT GAA AGA CTC				
Gly Lys Pro Ser Glu Lys Glu Cys Gly Pro His Glu Arg Leu				
140	150	160	170	
*	*	*	*	*
GAC TGT GGC AAC AAG AAG CCA TGC GAG CGC AAG TGC AAA ATA				
Asp Cys Gly Asn Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile				
180	190	200	210	
*	*	*	*	*
GAG ACA AGT GAG GAG GAT GAC TAC GAA GAG GGA ACC GAA				
Glu Thr Ser Glu Glu Asp Asp Tyr Glu Glu Gly Thr Glu				
220	230	240	250	
*	*	*	*	
CGT TTT CGA TGC CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA				
Arg Phe Arg Cys Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu				
260	270	280	290	
*	*	*	*	
TGC ATA TGC GAT GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA				
Cys Ile Cys Asp Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu				
300	310	320	330	340
*	*	*	*	*
TGT GTG ACT GAT GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT				
Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu Phe				
350	360	370	380	
*	*	*	*	
ATT ACT TTC GCA CCA TAA ACCCAATAAT GACCAATGAC TCCCATTCTT				
Ile Thr Phe Ala Pro				

Figure 13 A-2

390 400 410 420 430
* * * * *
CGTGATCAGC GTCGGTGGTT GACAGTCTCC CCTACATCTT AGTAGTTTG

440 450 460 470 480
* * * * *
CTTGATAATG TATACATAAA CTGTACTTTC TGAGATAGAA TAAAGCTCTC

490
*
AACTAC poly(A)

Figure 13 B-1 (AcaNAP24)

10	20	30	40	
*	*	*	*	
GAATTCCGCG GAATTCCGCA ACG ATG AAG ACG CTC TAT ATT ATC				
EcoRI Met Lys Thr Leu Tyr Ile Ile				
50	60	70	80	
*	*	*	*	
GCT ATA TGC TCG CTC CTC ATT TCG TTG TGT ACT GGA AGA CCG				
Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro				
90	100	110	120	
*	*	*	*	
GAA AAA AAG TGC GGT CCC GGT GAA AGA CTC GCC TGT GGC AAT				
Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Ala Cys Gly Asn				
130	140	150	160	170
*	*	*	*	*
AAG AAG CCA TGC GAG CGC AAG TGC AAA ATA GAG ACA AGT GAG				
Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu				
180	190	200	210	
*	*	*	*	
GAG GAG GAT GAC TAC CCA GAG GGA ACC GAA CGT TTT CGA TGC				
Glu Glu Asp Asp Tyr Pro Glu Gly Thr Glu Arg Phe Arg Cys				
220	230	240	250	
*	*	*	*	
CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA TGC ATA TGC GAT				
Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu Cys Ile Cys Asp				
260	270	280	290	
*	*	*	*	
GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT				
Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp				
300	310	320	330	
*	*	*	*	
GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA				
Asp Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala				
340	350	360	370	380
*	*	*	*	*
CCA TAA ACCCAATAAT GACCACTGGC TCCCCATTCTT CGTGACCAGC				
Pro				

Figure 13 B-2

390 400 410 420 430
* * * * *
GTCGGTGGTT GACAGTCTCC CCTGCATCTT AGTAGTTTG CTTGATAATG
440 450 460 470
* * * *
TATCCATAAA CAGTACTTTC TGAGATAGAA TAAAGCTCTC AACT poly(A)

Figure 13 C (AcaNAP25)

10 * 20 * 30 * 40 *
GAATTCCGTA CTACTCAACG ATG AAG ACG CTC TAT ATT ATC GCT
 EcoRI Met Lys Thr Leu Tyr Ile Ile Ala
 50 * 60 * 70 * 80 *
 ATA TGC TCG CTG CTC TTT TCA CTG TGT ACT GGA AGA CCG GAA
 Ile Cys Ser Leu Leu Phe Ser Leu Cys Thr Gly Arg Pro Glu
 90 * 100 * 110 * 120 *
 AAA AAG TGC GGT CCC GGT GAA AGA CTC GAC TGT GCC AAC AAG
 Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn Lys
 130 * 140 * 150 * 160 * 170 *
 AAG CCA TGC GAG CCC AAG TGC AAA ATA GAG ACA AGT GAG GAG
 Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu Glu
 180 * 190 * 200 * 210 *
 GAG GAT GAC GAC GTA GAG GAT ACC GAT GTG AGA TGC CTC GTA
 Glu Asp Asp Asp Val Glu Asp Thr Asp Val Arg Cys Leu Val
 220 * 230 * 240 * 250 *
 CGT GTG TGT GAA CGT CCT CTT AAA TGC ATA TGC AAG GAT GGA
 Arg Val Cys Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp Gly
 260 * 270 * 280 * 290 *
 TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT GAT GTA
 Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp Asp Val
 300 * 310 * 320 * 330 *
 TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA TAA
 Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro
 340 * 350 * 360 * 370 * 380 *
 ACCCAATAAT GACCACTGGC TCCCATTCTT CGTGATCAGC GTCGGTGGTT
 390 * 400 * 410 * 420 * 430 *
 GACAGTCTCC CCTGCATCTT AGTTGCTTTG CTTGATAATC TATACATAAA
 440 * 450 * 460 * 470 *
 CAGTACTTTC TGAGATAGAA TAAAGCTCTC AACT poly(A)

Figure 13 D-1 (AcaNAP31)

10	20	30	40	50
*	*	*	*	*
<u>GAATTCCGGA</u> CTTACTAGTA CTCAGCGAAT CAAATACGAC TTACTACTAC				
EcoRI				
60	70	80	90	
*	*	*	*	
TCAACG ATG AAG ACG CTC TCT GCT ATC CCT ATA ATG CTG CTC				
Met Lys Thr Leu Ser Ala Ile Pro Ile Met Leu Leu				
100	110	120	130	
*	*	*	*	
CTG GTA TCG CAA TGC AGT GGA AAA TCA CTG TGG GAT CAG AAG				
Leu Val Ser Gln Cys Ser Gly Lys Ser Leu Trp Asp Gln Lys				
140	150	160	170	
*	*	*	*	
TGT GGT GAG AAT GAA AGG CTC GAC TGT GGC AAT CAG AAG GAC				
Cys Gly Glu Asn Glu Arg Leu Asp Cys Gly Asn Gln Lys Asp				
180	190	200	210	
*	*	*	*	
TGT GAG CGC AAG TGC GAT GAT AAA AGA AGT GAA GAA GAA ATT				
Cys Glu Arg Lys Cys Asp Asp Lys Arg Ser Glu Glu Glu Ile				
220	230	240	250	260
*	*	*	*	*
ATG CAG GCA TGT CTC ACA CGT CAA TGT CTT CCT CCT GTT TGC				
Met Gln Ala Cys Leu Thr Arg Gln Cys Leu Pro Pro Val Cys				
270	280	290	300	
*	*	*	*	
GTA TGT GAA GAT GGA TTC FAC AGA AAT GAC AAC GAC CAA TGT				
Val Cys Glu Asp Gly Phe Tyr Arg Asn Asp Asn Gln Cys				
310	320	330	340	
*	*	*	*	
GTT GAT GAA GAA GAA TGC AAT ATG GAG TTT ATT ACT TTC GCA				
Val Asp Glu Glu Glu Cys Asn Met Glu Phe Ile Thr Phe Ala				
350	360	370	380	390
*	*	*	*	*
CCA TGA AGCAAATGAC AGCCGATGGT TTGGACTCTC GCTACAGATC				
Pro				
400	410	420	430	440
*	*	*	*	*
ACAGCTTAC TGTTCCCTT GCATCATAGT AGTTTGCTA GATAGTGTAT				

Figure 13 D-2

450 * 460 * 470 * 480 *
ATATTAGCAT GATTTCCTGA TAGGGAGAAT AAAGCTTC AATTTTC
poly(A)

Figure 13 E-1 (AcaNAP44)

10	20	30	40	
*	*	*	*	
<u>GAATTCCGGCG</u>	GAATTCCGCA	ACG ATG AAG ACG CTC TAT ATT ATC		
EcoRI		Met Lys Thr Leu Tyr Ile Ile		
50	60	70	80	
*	*	*	*	
GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT GGA AGA CCG				
Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro				
90	100	110	120	
*	*	*	*	
GAA AAA AAG TGC GGT CCC GGT GAA AGA CTC GAC TGT GCC AAC				
Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn				
130	140	150	160	170
*	*	*	*	*
AAG AAG CCA TGC GAG CCC AAG TGC AAA ATA GAG ACA AGT GAG				
Lys Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu				
180	190	200	210	
*	*	*	*	*
GAG GAG GAT GAC GAC GTA GAG GAA ACC GAT GTG AGA TGC CTC				
Glu Glu Asp Asp Asp Val Glu Glu Thr Asp Val Arg Cys Leu				
220	230	240	250	
*	*	*	*	*
GTA CGT GTG TGT GAA CGG CCT CTT AAA TGC ATA TGC AAG GAT				
Val Arg Val Cys Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp				
260	270	280	290	
*	*	*	*	*
GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT GAT				
Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp Asp				
300	310	320	330	
*	*	*	*	*
GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA				
Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro				
340	350	360	370	380
*	*	*	*	*
TAA ACCCAATAAT GACCACTGGC TCCCCATTCTT CGTGATCAGC				
390	400	410	420	430
*	*	*	*	*
GTCGGTGGTT GACAGTCTCC CCTGCATCTT AGTTGCTTTG CTTGATAATC				

Figure 13 E-2

440 450 460 470
* * * *
TATAACATAAA CAGTACTTTC TGAGATAGAA TAAAGCTCTC AACTAC
poly(A)

Figure 13 F-1 (AcaNAP45)

10 * 20 * 30 * 40 *
GAATTCCGGA AAA ATG CTG ATG CTC TAC CTT GTT CCT ATC TGG
 EcoRI Met Leu Met Leu Tyr Leu Val Pro Ile Trp
 50 * 60 * 70 * 80 *
 TTG CTA CTC ATT TCG CAA TGC AGT GGA AAA TCC GCG AAG AAA
 Leu Leu Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys Lys
 90 * 100 * 110 * 120 *
 TGT GGT CTC AAT GAA AAA TTG GAC TGT GGC AAT CTG AAG GCA
 Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala
 130 * 140 * 150 * 160 *
 TGC GAG AAA AAG TGC AGC GAC TTG GAC AAT GAG GAG GAT TAT
 Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp Tyr
 170 * 180 * 190 * 200 * 210 *
 AAG GAG GAA GAT GAG TCG AAA TGC CGA TCA CGT GAA TGT AGT
 Lys Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser
 220 * 230 * 240 * 250 *
 CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC TAC AGA AAC AAG
 Arg Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys
 260 * 270 * 280 * 290 *
 AAG GGC CAA TGT GTG ACA AGA GAT GAT TGC GAG TAT GAC AAT
 Lys Gly Gln Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn
 300 * 310 * 320 * 330 *
 ATG GAG ATT ATC ACT TTT CCA CCA GAA GAT AAA TGT GGT CCC
 Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Lys Cys Gly Pro
 340 * 350 * 360 * 370 *
 GAT GAA TGG TTC GAC TGG TGT GGA ACT TAC AAG CAG TGT GAG
 Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys Gln Cys Glu
 380 * 390 * 400 * 410 * 420 *
 CGC AAG TGC AAT AAG GAG CTA AGT GAG AAA GAT GAA GAG GCA
 Arg Lys Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Glu Ala

Figure 13 F-2

430 440 450 460
 * * * *
 TGC CTC TCA CGT GCT TGT ACT GGT CGT GCT TGT GTT TGC AAC
 Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Asn

 470 480 490 500
 * * * *
 GAC GGA CTG TAC AGA GAC GAT TTT GGC AAT TGT GTT GAG AAA
 Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu Lys

 510 520 530 540
 * * * *
 GAC GAA TGT AAC GAT ATG GAG ATT ATC ACT TTT CCA CCG GAA
 Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu

 550 560 570 580
 * * * *
 ACC AAA CAC TGA CCAAAGGCTC TAACTCTCGC TACATAACGT
 Thr Lys His

 590 600 610 620 630
 * * * * *
 CAGTGCTTGA ATTGCCCTT TACGAGTTAG TAATTTGAC TAACTCTGTG

 640 650 660 670 680
 * * * * *
 TAATTGAGCA TTGTCTACTG ATGGTGAAAA TGAAGTGTTC AATGTCT
 poly(A)

Figure 13 G-1 (AcaNAP47)

10 * 20 * 30 * 40 *
GAATTCCGCG GAATTCCGGT TGGCGGCAGA AAA ATG CTG ATG CTC
 EcoRI Met Leu Met Leu
 50 * 60 * 70 * 80 *
 TAC CTT GTT CCT ATC TGG TTC CTG CTC ATT TCG CAA TGC AGT
 Tyr Leu Val Pro Ile Trp Phe Leu Leu Ile Ser Gln Cys Ser
 90 * 100 * 110 * 120 *
 GGA AAA TCC GCG AAG AAA TGT GGC CTC AAT GAA AAA TTG GAC
 Gly Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp
 130 * 140 * 150 * 160 * 170 *
 TGT GGC AAT CTG AAG GCA TGC GAG AAA AAG TGC AGC GAC TTG
 Cys Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu
 180 * 190 * 200 * 210 *
 GAC AAT GAG GAG GAT TAT GGG GAG GAA GAT GAG TCG AAA TGC
 Asp Asn Glu Glu Asp Tyr Gly Glu Asp Glu Ser Lys Cys
 220 * 230 * 240 * 250 *
 CGA TCA CGT GAA TGT ATT GGT CGT GTT TGC GTA TGC GAT GAA
 Arg Ser Arg Glu Cys Ile Gly Arg Val Cys Val Cys Asp Glu
 260 * 270 * 280 * 290 *
 GGA TTC TAC AGA AAC AAG AAG GGC CAA TGT GTG ACA AGA GAC
 Gly Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp
 300 * 310 * 320 * 330 *
 GAT TGC GAG TAT GAC AAT ATG GAG ATT ATC ACT TTT CCA CCA
 Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro
 340 * 350 * 360 * 370 * 380 *
 GAA GAT AAA TGT GGT CCC GAT GAA TGG TTC GAC TGG TGT GGA
 Glu Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly
 390 * 400 * 410 * 420 *
 ACT TAC AAG CAG TGT GAG CGC AAG TGC AGT GAG GAG CTA AGT
 Thr Tyr Lys Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser

Figure 13 G-2

430 * 440 * 450 * 460 *
 GAG AAA AAT GAG GAG GCA TGC CTC TCA CGT GCT TGT ACT GGT
 Glu Lys Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly

 470 * 480 * 490 * 500 *
 CGT GCT TGC GTT TGC AAC GAC GGA TTG TAT AGA GAC GAT TTT
 Arg Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Asp Phe

 510 * 520 * 530 * 540 *
 GGC AAT TGT GTT GAG AAA GAC GAA TGT AAC GAT ATG GAG ATT
 Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile

 550 * 560 * 570 * 580 *
 ATC ACT TTT CCA CCG GAA ACC AAA CAC TGA CCAAAGGCTC
 Ile Thr Phe Pro Pro Glu Thr Lys His

 590 * 600 * 610 * 620 * 630 *
 TAGCTCTCGC TACATAACGT CAGTGCTTGA ATTGTCCCTT TACGTGTTAG

 640 * 650 * 660 * 670 * 680 *
 TAATTTGAC TAACTCTGTG TATTGAGCA TTGTCTACTA ATGGTGAAAA

 690 * 700 *
 TGAAGCTTTT CAATGACT poly(A)

Figure 13 H-1 (AcaNAP48)

10 * 20 * 30 * 40 *
GAATTCCGTA CGACCTACTA CTACTCAACG ATG AAG GCG CTC TAT
 EcoRI Met Lys Ala Leu Tyr
 50 * 60 * 70 * 80 *
 GTT ATC TCT ATA ACG TTG CTC CTG GTA TGG CAA TGC AGT GCA
 Val Ile Ser Ile Thr Leu Leu Leu Val Trp Gln Cys Ser Ala
 90 * 100 * 110 * 120 *
 AGA ACA GCG AGG AAA CCC CCA ACG TGT GGT GAA AAT GAA AGG
 Arg Thr Ala Arg Lys Pro Pro Thr Cys Gly Glu Asn Glu Arg
 130 * 140 * 150 * 160 * 170 *
 GTC GAA TGG TGT GGC AAG CAG TGC GAG ATC ACA TGT GAC GAC
 Val Glu Trp Cys Gly Lys Gln Cys Glu Ile Thr Cys Asp Asp
 180 * 190 * 200 * 210 *
 CCA GAT AAG ATA TGC CGC TCA CTC GCT TGT CCT GGT CCT CCT
 Pro Asp Lys Ile Cys Arg Ser Leu Ala Cys Pro Gly Pro Pro
 220 * 230 * 240 * 250 *
 GCT TGC GTA TGC GAC GAC GGA TAC TAC AGA GAC ACG AAC GTT
 Ala Cys Val Cys Asp Asp Gly Tyr Tyr Arg Asp Thr Asn Val
 260 * 270 * 280 * 290 *
 GGC TTG TGT GTA CAA TAT GAC GAA TGC AAC GAT ATG GAT ATT
 Gly Leu Cys Val Gln Tyr Asp Glu Cys Asn Asp Met Asp Ile
 300 * 310 * 320 * 330 * 340 *
 ATT ATG GTT TCA TAG GGTTGACTGA AGAATCGAAC AACCGGTGCA
 Ile Met Val Ser
 350 * 360 * 370 * 380 * 390 *
 CAACTTCTAT GCTTGACTAT CTCTCTTGCA TCATGCAAGT TTAGCTAGAT
 400 * 410 * 420 * 430 * 440 *
 AGTGTATATA TTAGCAAGAC CCCTTGGGGA GAATGAAGCT TCCCAACTAT
 450 * 460 * 470 * 480 * 490 *
 ATTAAATCAA TAACGTTTC GCTTCATGTA CACGTGCTCA GCACATTCA

Figure 13 H-2

500

*

510

*

520

*

ATCCACTCCT CACACTCCAT GAAAGCAGTG AAATGTT poly(A)

Figure 14

10 20 30 40
 * * * *
 GCC AAC TCT TCG AAC ATG ATT CGA GGC CTC GTT CTT CTT TCT CTC CTG
 Met Ile Arg Gly Leu Val Leu Leu Ser Leu Leu>

 50 60 70 80 90
 * * * * *
 TTT TGC GTC ACT TTT GCA GCG AAG AGA GAT TGT CCA GCA AAT GAG GAA
 Phe Cys Val Thr Phe Ala Ala Lys Arg Asp Cys Pro Ala Asn Glu Glu>

 100 110 120 130 140
 * * * * *
 TGG AGG GAA TGT GGC ACT CCA TGT GAA CCA AAA TGC AAT CAA CCG ATG
 Trp Arg Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Gln Pro Met>

 150 160 170 180 190
 * * * * *
 CCA GAT ATA TGT ACT ATG AAT TGT ATC GTC GAT GTG TGT CAA TGC AAG
 Pro Asp Ile Cys Thr Met Asn Cys Ile Val Asp Val Cys Gln Cys Lys>

 200 210 220 230 240
 * * * * *
 GAG GGA TAC AAG CGT CAT GAA ACG AAG GGA TGC TTA AAG GAA GGA TCA
 Glu Gly Tyr Lys Arg His Glu Thr Lys Gly Cys Leu Lys Glu Gly Ser>

 250 260 270 280
 * * * *
 GCT GAT TGT AAA TAA GTT ATC AGA ACG CTC GTT TTG TCT TAC ATT AGA
 Ala Asp Cys Lys ***

 290 300 310 320 330
 * * * * *
 TGG GTG AGC TGA TGT ATC TGT CAG ATA AAC TCT TTC TTC TAA AAA AAA

 340 350 360
 * * *
 AAA AAA AAA AAA AAA AAA AAA A

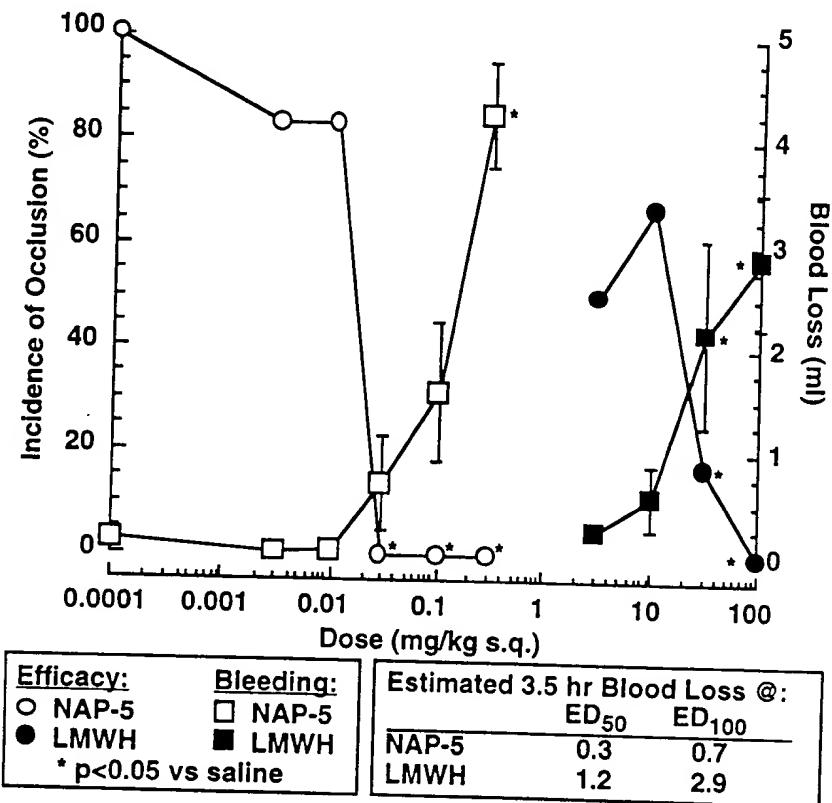
FIGURE 15

FIGURE 16

Figure 17

Lys Pro Asn Asn Val Met Thr Asn Ala **Cys** Gly Leu Asn Glu
 1 5 10

Tyr Phe Ala Glu **Cys** Gly Asn Met Lys Glu **Cys** Glu His Arg
 15 20 25

Cys Asn Glu Glu Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile
 30 35 40

Thr Ala **Cys** Leu Ile Arg Val **Cys** Phe Arg Pro Gly Ala **Cys**
 45 50 55

Val **Cys** Lys Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser **Cys**
 60 65 70

Val Glu Glu Asp Asp **Cys** Glu Tyr Glu Asn Met Glu Phe Ile
 75 80

Thr Phe Ala Pro Glu Val Pro Ile **Cys** Gly Ser Asn Glu Arg
 85 90 95

Tyr Ser Asp **Cys** Gly Asn Asp Lys Gln **Cys** Glu Arg Lys **Cys**
 100 105 110

Asn Glu Asp Asp Tyr Glu Lys Gly Asp Glu Ala **Cys** Arg Ser
 115 120 125

His Val **Cys** Glu Arg Pro Gly Ala **Cys** Val **Cys** Glu Asp Gly
 130 135 140

Phe Tyr Arg Asn Lys Lys Gly Ser **Cys** Val Glu Ser Asp Asp
 145 150

Cys Glu Tyr Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu
 155 160 165

Thr Ser Arg
 170

Figure 18

Lys Ser Ala Lys Lys **Cys** Gly Leu Asn Glu Lys Leu Asp **Cys**
 1 5 10

Gly Asn Leu Lys Ala **Cys** Glu Lys Lys **Cys** Ser Asp Leu Asp
 15 20 25

Asn Glu Glu Asp Tyr Lys Glu Glu Asp Glu Ser Lys **Cys** Arg
 30 35 40

Ser Arg Glu **Cys** Ser Arg Arg Val **Cys** Val **Cys** Asp Glu Gly
 45 50 55

Phe Tyr Arg Asn Lys Lys Gly Gln **Cys** Val Thr Arg Asp Asp
 60 65 70

Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
 75 80

Asp Lys **Cys** Gly Pro Asp Glu Trp Phe Asp Trp **Cys** Gly Thr
 85 90 95

Tyr Lys Gln **Cys** Glu Arg Lys **Cys** Asn Lys Glu Leu Ser Glu
 100 105 110

Lys Asp Glu Glu Ala **Cys** Leu Ser Arg Ala **Cys** Thr Gly Arg
 115 120 125

Ala **Cys** Val **Cys** Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly
 130 135 140

Asn **Cys** Val Glu Lys Asp Glu **Cys** Asn Asp Met Glu Ile Ile
 145 150

Thr Phe Pro Pro Glu Thr Lys His
 155 160

Figure 19

Lys Ser Ala Lys Lys **Cys** Gly Leu Asn Glu Lys Leu Asp **Cys**
 1 5 10

Gly Asn Leu Lys Ala **Cys** Glu Lys Lys **Cys** Ser Asp Leu Asp
 15 20 25

Asn Glu Glu Asp Tyr Gly Glu Glu Asp Glu Ser Lys **Cys** Arg
 30 35 40

Ser Arg Glu **Cys** Ile Gly Arg Val **Cys** Val **Cys** Asp Glu Gly
 45 50 55

Phe Tyr Arg Asn Lys Lys Gly Gln **Cys** Val Thr Arg Asp Asp
 60 65 70

Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
 75 80

Asp Lys **Cys** Gly Pro Asp Glu Trp Phe Asp Trp **Cys** Gly Thr
 85 90 95

Tyr Lys Gln **Cys** Glu Arg Lys **Cys** Ser Glu Glu Leu Ser Glu
 100 105 110

Lys Asn Glu Glu Ala **Cys** Leu Ser Arg Ala **Cys** Thr Gly Arg
 115 120 125

Ala **Cys** Val **Cys** Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly
 130 135 140

Asn **Cys** Val Glu Lys Asp Glu **Cys** Asn Asp Met Glu Ile Ile
 145 150

Thr Phe Pro Pro Glu Thr Lys His
 155 160

Figure 20

Lys Ala Ala Lys Lys **Cys** Gly Leu Asn Glu Arg Leu Asp **Cys**
1 5 10

Gly Asn Leu Lys Gln **Cys** Glu Pro Lys **Cys** Ser Asp Leu Glu
15 20 25

Ser Glu Glu Tyr Glu Glu Glu Asp Glu Ser Lys **Cys** Arg Ser
30 35 40

Arg Glu **Cys** Ser Arg Arg Val **Cys** Val **Cys** Asp Glu Gly Phe
45 50 55

Tyr Arg Asn Lys Lys Gly Lys **Cys** Val Ala Lys Asp Val **Cys**
60 65 70

Glu Asp Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp
75 80

Glu **Cys** Gly Pro Asp Glu Trp Phe Asp Tyr **Cys** Gly Asn Tyr
85 90 95

Lys Lys **Cys** Glu Arg Lys **Cys** Ser Glu Glu Thr Ser Glu Lys
100 105 110

Asn Glu Glu Ala **Cys** Leu Ser Arg Ala **Cys** Thr Gly Arg Ala
115 120 125

Cys Val **Cys** Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn
130 135 140

Cys Val Pro His Asp Glu **Cys** Asn Asp Met Glu Ile Ile Thr
145 150

Phe Pro Pro Glu Thr Lys His
155 160